CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/535,522_   CRF Edit Date: _6/2/05_
Edited by: _AL_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

✓ Corrected the SEQ ID NO. Sequence numbers edited were:

_10_

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

/ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

✓ Inserted mandatory headings/numeric identifiers, specifically:

<220> in Seqs. 8, 10

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

PCT

RAW SEQUENCE LISTING   DATE: 06/02/2005
PATENT APPLICATION: US/10/535,522   TIME: 14:09:45

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\06022005\J535522.raw**

```
      3 <110> APPLICANT: Steinkasserer, Alexander
      5 <120> TITLE OF INVENTION: Use of Soluble Forms of CD83 and Nucleic Acids Encoding
      6       them for the Treatment or Prevention of Diseases
W-->  7 <130> FILE REFERENCE: 032723woJH
W-->  8 <140> CURRENT APPLICATION NUMBER:
C-->  9 <141> CURRENT FILING DATE: 2005-05-18
W--> 10 <160> NUMBER OF SEQ ID: 12
     11 <170> SOFTWARE: PatentIn Ver. 2.1
     14 <210> SEQ ID NO: 1
     15 <211> LENGTH: 618
     16 <212> TYPE: DNA
     17 <213> ORGANISM: Homo sapiens
W--> 18 <220> FEATURE:
     19 <221> NAME/KEY: CDS
     20 <222> LOCATION: (1)..(615)
     22 <400> SEQUENCE: 1
     23 atg tcg cgc ggc ctc cag ctt ctg ctc ctg agc tgc gcc tac agc ctg      48
     24 Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
     25  1               5                  10                  15
     27 gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac      96
     28 Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
     29              20                  25                  30
     31 ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc     144
     32 Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
     33              35                  40                  45
     35 tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag     192
     36 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
     37      50                  55                  60
     39 gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt     240
     40 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
     41  65                  70                  75                  80
     43 tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac     288
     44 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
     45                  85                  90                  95
     47 act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg     336
     48 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
     49              100                 105                 110
     51 gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga     384
     52 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
     53              115                 120                 125
     56 tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag     432
     57 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
     58      130                 135                 140
```

RAW SEQUENCE LISTING   DATE: 06/02/2005
PATENT APPLICATION: **US/10/535,522**   TIME: 14:09:45

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\06022005\J535522.raw**

```
60 att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att     480
61 Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
62 145                 150                 155                 160
64 ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct     528
65 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
66                 165                 170                 175
68 aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag     576
69 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
70                 180                 185                 190
72 cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga             618
73 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
74         195                 200                 205
```

```
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 205
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2
83 Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
84   1                 5                  10                  15
86 Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
87                 20                  25                  30
89 Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
90         35                  40                  45
92 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
93     50                  55                  60
95 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
96   65                  70                  75                  80
98 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
99                 85                  90                  95
101 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
102                 100                 105                 110
104 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
105         115                 120                 125
107 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
108     130                 135                 140
111 Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
112 145                 150                 155                 160
114 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
115                 165                 170                 175
117 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
118                 180                 185                 190
120 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
121         195                 200                 205
```

```
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 2051
126 <212> TYPE: DNA
127 <213> ORGANISM: Mus musculus
```
W--> `128 <220> **FEATURE:**`
```
129 <221> NAME/KEY: CDS
```

RAW SEQUENCE LISTING   DATE: 06/02/2005
PATENT APPLICATION: US/10/535,522   TIME: 14:09:45

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\06022005\J535522.raw**

```
130 <222> LOCATION: (14)..(601)
132 <400> SEQUENCE: 3
133 gcgctccagc cgc atg tcg caa ggc ctc cag ctc ctg ttt cta ggc tgc     49
134             Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
135              1               5                   10
137 gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct     97
138 Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
139         15                  20                  25
141 tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag    145
142 Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
143         30                  35                  40
145 ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag    193
146 Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
147 45                  50                  55                  60
149 agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc    241
150 Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
151                 65                  70                  75
153 agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc    289
154 Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
155         80                  85                  90
157 tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac    337
158 Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
159         95                  100                 105
161 ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct    385
162 Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
163     110                 115                 120
165 aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc    433
166 Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
167 125                 130                 135                 140
169 tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt    481
170 Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
171                 145                 150                 155
173 gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa    529
174 Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
175         160                 165                 170
177 caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg    577
178 Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
179         175                 180                 185
183 acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaaag  631
184 Thr Leu Pro Lys Thr Glu Thr Val
185     190                 195
187 ccaagggcac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc  691
189 atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc  751
191 cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct  811
193 ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgcttttca  871
195 gtcatctaca agctatggtg agatgcaggt gaagcagggt catgggaaat ttgaacactc  931
197 tgagctggcc ctgtgacaga ctcctgagga cagctgtcct ctcctacatc tgggatacat  991
199 ctctttgaat ttgtcctgtt tcgttgcacc agcccagatg tctcacatct ggcggaaatt  1051
201 gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt  1111
```

```
203 cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc 1171
205 cagcagggcc tttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca 1231
207 catttatttt tttaatcttc atgtacttgt caaagaagaa tttttcatgt tttttcaaag 1291
209 aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga 1351
211 caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca 1411
213 ctgtacagtg ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471
215 aagattgtct gtatgattct ggacgagtca cttgtggttt tcactctctg gttagtaaac 1531
217 cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591
219 tagtgaatac attggcaact ctactgggct gttaccttgt tgatatccta gagttctgga 1651
221 gctgagcgaa tgcctgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa 1711
223 aaaggacatg agcatggtct tctgtgtgaa ctcctcctga gaaacgtgga gactggctca 1771
225 gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831
227 tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891
229 taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatggtgt 1951
231 gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011
233 tcagccatga ctttcatgct attaaaagaa tgcatgtgaa                        2051
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 196
238 <212> TYPE: PRT
239 <213> ORGANISM: Mus musculus
241 <400> SEQUENCE: 4
242 Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
243  1                5                  10                  15
245 Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
246              20                  25                  30
248 Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
249          35                  40                  45
251 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
252      50                  55                  60
254 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
255  65                  70                  75                  80
257 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
258                  85                  90                  95
260 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
261              100                 105                 110
263 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
264          115                 120                 125
266 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
267      130                 135                 140
269 Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
270 145                 150                 155                 160
272 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
273                  165                 170                 175
275 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
276              180                 185                 190
278 Thr Glu Thr Val
279          195
282 <210> SEQ ID NO: 5
283 <211> LENGTH: 31
```

RAW SEQUENCE LISTING   DATE: 06/02/2005
PATENT APPLICATION: US/10/535,522   TIME: 14:09:45

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\06022005\J535522.raw**

```
    284 <212> TYPE: DNA
    285 <213> ORGANISM: Artificial Sequence
W--> 286 <220> FEATURE:
    287 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for CD83ext
    289 <400> SEQUENCE: 5
    290 tcccccggga acgccggagg tgaaggtggc t                             31
    293 <210> SEQ ID NO: 6
    294 <211> LENGTH: 31
    295 <212> TYPE: DNA
    296 <213> ORGANISM: Artificial Sequence
W--> 297 <220> FEATURE:
    298 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for CD83ext
    300 <400> SEQUENCE: 6
    301 aattagaatt ctcaaatctc cgctctgtat t                             31
    304 <210> SEQ ID NO: 7
    305 <211> LENGTH: 435
    306 <212> TYPE: DNA
    307 <213> ORGANISM: Artificial Sequence
W--> 308 <220> FEATURE:
    309 <223> OTHER INFORMATION: Description of Artificial Sequence: partial
    310         sequence of pGEX2ThCD83ext
W--> 311 <220> FEATURE:
    312 <221> NAME/KEY: CDS
    313 <222> LOCATION: (1)..(417)
W--> 314 <220> FEATURE:
    315 <221> NAME/KEY: mat_peptide
    316 <222> LOCATION: (28)..(417)
    318 <400> SEQUENCE: 7
    319 cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag    48
    320 Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
    321               -5              -1  1                   5
    323 gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc    96
    324 Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
    325          10              15                  20
    327 tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag   144
    328 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
    329      25                  30                  35
    331 ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga   192
    332 Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
    333  40              45                  50                  55
    335 cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat   240
    336 Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
    337              60                  65                  70
    339 gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg   288
    340 Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
    341          75                  80                  85
    343 ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta   336
    344 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
    345          90                  95                  100
```

VERIFICATION SUMMARY   DATE: 06/02/2005
PATENT APPLICATION: **US/10/535,522**   TIME: 14:09:46

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\06022005\J535522.raw**

```
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:283 W: Missing Blank Line separator, <160> field identifier
L:18 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <220> field identifier
L:286 M:283 W: Missing Blank Line separator, <220> field identifier
L:297 M:283 W: Missing Blank Line separator, <220> field identifier
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:311 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:283 W: Missing Blank Line separator, <220> field identifier
L:398 M:283 W: Missing Blank Line separator, <220> field identifier
L:401 M:283 W: Missing Blank Line separator, <220> field identifier
L:404 M:283 W: Missing Blank Line separator, <220> field identifier
L:450 M:283 W: Missing Blank Line separator, <220> field identifier
L:489 M:283 W: Missing Blank Line separator, <220> field identifier
L:501 M:283 W: Missing Blank Line separator, <220> field identifier
```